

Table 3. Comparison of the top 20 liquid-associated pairs (LAPs) scouted by CMD1 and CMK1

Top 10 positive LAPs scouted by CMD1	Top 11–20 LAPs scouted by CMD1	Top 10 negative LAPs scouted by CMD1	Top 11–20 LAPs scouted By CMD1
RIM13 TFC8 UFD2 YML118W OPY1 KAR4 YER037W MRS2 YBL101WA LRS4 YBR012WA RIM13 DOC1 SOK2 YGL149W YLR365W YER182W MRPL40 YER037W SSP1	YJL067W MRPL40 YER037W YNL234W TEC1 RML2 STL1 YNL083W YBL107C COX5B DOC1 YPL136W IME4 YPL126W GLT1 YNR076W HIS4 YGL107C YLR366W PHA2	RRM3 YJL021C YCR076C OYE3 RML2 YLR331C HEX3 YPL134C AMD1 YOL010W YKL175W TFC8 SSA3 YBT1 YAL004W YLL023C CCT2 YNL094W RML2 YOL046C	YML118W YOL075C YAL028W YLL023C YDR459C KAR2 YAP6 YPR117W YGL165C SEC21 YLR454W YPL186C IME1 YNL180C PTP3 YNL134C YKL075C COQ2 YGL064C KAP120
Top 10 positive LAPs scouted by CMK1	Top 11–20 LAPs scouted by CMK1	Top 10 negative LAPs scouted by CMK1	Top 11–20 LAPs scouted by CMK1
YDR278C YPL006W YBR095C ERF2 IME1 YNR071C YBR159W USO1	YBR144C YDL024C OPY1 RRP45 YHR198C CDA2 NUF1 YGL149W	USO1 MUC1 SXM1 YPR117W HXT14 YOR243C PTC1 YHR116W	YCR024A NPR2 LCB2 YGR150C YGR090W MUC1 YAL004W MET6

YDR278C YPR117W	YHR035W YMR206W	DED81 YMR258C	CDA2 MAS6
NEO1 YOR304W	APN2 PRP31	CEG1 YKL155C	SXM1 MUC1
HTA2 YJR072C	SOR1 AXL1	PFK1 YMR258C	YDR078C CCT2
YDR278C YPL088W	SDL1 MUC1	SIP4 KHA1	YGL002W PMU1
YLR296W RIM13	TFC8 YPR083W	PHO5 NPR2	MNR2 YNL247W
MUC1 YJL160C	YDL015C LRS4	YGR054W MUC1	YDL172C YHL018W

Nine shared genes are colored in red. One of them, an unknown gene, *YGL149W*, is paired with *NUF1*, an essential target of calmodulin, in a positive LAP of *CMK1*. In another LAP table for *YGL149W*, *SSK2* (MAP kinase kinase kinase, HOG pathway) is scouted five times. The 13 blue-colored genes in this table together with *IME1*, *RIM13*, and *OPY1*, depict the convergence of various signal transduction pathways of growth morphogenesis. *YGL149W* has protein–protein interaction with CRM1, beta-karyopherin, functionin exporting certain protein from nucleus; CRM1 also interacts with NUF1. Two beta-karyopherin proteins (*KAP120* and *SXM1*) also appear in the LAPs of CMD1.

TFC8 RNA POLYMERASE III TRANSCRIPTION INITIATION FACTOR TFIIC TAU 60 KDA SUBUNIT
LRS4 INVOLVED IN RDNA SILENCING
OPY1 PHEROMONE RESISTANT YEAST 1
RIM13 CALPAIN LIKE CYSTEINE PROTEASE ; sporulation
IME1 TRANSCRIPTION FACTOR REQUIRED FOR SPORULATION
CCT2 CHAPERONIN OF THE TCP1 RING COMPLEX CYTOSOLIC
NUF1 SPINDLE POLE BODY COMPONENT
PTP3 PROTEIN TYROSINE PHOSPHATASE involved in Hog1p MAP kinase high osmolarity sensing
pathwas and Fus3p MAPK pheromone response pathway
PTC1 PROTEIN SERINE/THREONINE PHOSPHATASE 2C
SOK2 REGULATORY PROTEIN IN THE PKA SIGNAL TRANSDUCTION PATHWAY, camp dependent
kinase stimulated growth, pseudohyphal differentiation and sporulation
MUC1 EXTRACELLULAR ALPHA 1 4 GLUCAN GLUCOSIDASE; pseudohyphal growth
TEC1 TY TRANSCRIPTION ACTIVATOR; involved with STE12 in pseudohyphal growth
SIP4 transcriptional activator, activated by SNF1 PROTEIN KINASE
CDA2 SPORULATION SPECIFIC CHITIN DEACETYLASE
IME4 POSITIVE TRANSCRIPTION FACTOR FOR IME2
SSP1 ESSENTIAL FOR MEIOSIS AND SPORE FORMATION
KAR4 REGULATORY PROTEIN REQUIRED FOR PHEROMONE INDUCTION OF KARYOGAMY GENES
KAR2 NUCLEAR FUSION PROTEIN
DOC1 COMPONENT OF THE ANAPHASE PROMOTING COMPLEX
AXL1 PROTEASE; second proteolytic step of a factor N terminal processing, pheromone response
morphogenesis, bud site seclction
ERF2 PROTEIN INVOLVED IN PALMITOYLATION AND LOCALIZATION OF RAS2P
KAP120 NUCLEAR TRANSPORT FACTOR MEMBER OF KARYOPHERIN BETA FAMILY
SXM1 PUTATIVE BETA KARYOPHERIN

SSA3 HEAT SHOCK PROTEIN OF HSP70 FAMILY CYTOSOLIC
YAP6 TRANSCRIPTION FACTOR OF A FUNGAL SPECIFIC FAMILY OF BZIP PROTEINS
RRM3 DNA HELICASE INVOLVED IN RDNA REPLICATION AND TY1 TRANSPOSITION
 RML2 RIBOSOMAL L2 PROTEIN MITOCHONDRIAL
 MRPL40 RIBOSOMAL PROTEIN OF THE LARGE SUBUNIT **YML40** MITOCHONDRIAL
 MAS6 MITOCHONDRIAL INNER MEMBRANE IMPORT TRANSLOCASE SUBUNIT
 MRS2 RNA SPLICING PROTEIN AND MEMBER OF THE MITOCHONDRIAL CARRIER FAMILY **MCF**
 USO1 protein transport from ER to Golgi
 SEC21 COATOMER COMPLEX GAMMA CHAIN **GAMMA COP** OF SECRETORY PATHWAY VESICLES
 YBT1 YEAST BILE TRANSPORTER
 STL1 member of hexose transporter family
 HEX3 HEXOSE METABOLISM RELATED PROTEIN
 HXT14 HEXOSE TRANSPORT PROTEIN
 APN2 AP ENDONUCLEASE EXONUCLEASE III HOMOLOG; DNA repair
 DED81 ASPARAGINYL TRNA SYNTHETASE
 CYSTEINYL TRNA SYNTHETASE
 CEG1 MRNA GUANYLYLTRANSFERASE **MRNA CAPPING ENZYME ALPHA SUBUNIT**
 PRP31 PRE MRNA SPLICING PROTEIN
 RRP45 RRNA PROCESSING PROTEIN
 HTA2 HISTONE H2A.2
 LCB2 SERINE C PALMITOYLTRANSFERASE SUBUNIT
 PHA2 PREPHENATE DEHYDRATASE
 HIS4 PHOSPHORIBOSYL AMP CYCLOHYDROLASE/PHOSPHORIBOSYL ATP PYROPHOSPHATASE/HISTIDINOL
 DEHYDROGENASE
 SOR1 SORBITOL DEHYDROGENASE
 MET6 5 METHYLTETRAHYDROPTEROYLTRIGLUTAMATE HOMOCYSTEINE METHYLTRANSFERASE
 PFK1 6 PHOSPHOFRUCTOKINASE ALPHA SUBUNIT
 GLT1 GLUTAMATE SYNTHASE **NAPDPH** **GOGAT**
 OYE3 NAPDH DEHYDROGENASE, OLD YELLOW ENZYME, ISOFORM 3
 AMD1 AMP DEAMINASE
 SDL1 STRONG SIMILARITY TO L SERINE DEHYDRATASE CHA1P
 COX5B CYTOCHROME C OXIDASE CHAIN VB
 COQ2 PARA HYDROXYBENZOATE POLYPRENYLTRANSFERASE
 UFD2 UBIQUITIN FUSION DEGRADATION PROTEIN
 NEO1 SIMILARITY TO AMINO PHOSPHOLIPIDS ATPASE DRS2P
 KHA1 K⁺/H⁺ EXCHANGER
 PHO5 REPRESSIBLE ACID PHOSPHATASE PRECURSOR
 NPR2 NITROGEN PERMEASE REGULATOR
 MNR2 OVEREXPRESSION OVERCOMES MANGANESE TOXICITY
 PMU1 HIGH COPY SUPPRESSOR OF TS TPS2 MUTANT PHENOTYPE